



RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 09/208,629G
Source: 1600
Date Processed by STIC: 3/17/04

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<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 10/08/03



1600

RAW SEQUENCE LISTING

DATE: 03/17/2004

PATENT APPLICATION: US/09/208,629G

TIME: 15:54:21

Input Set : A:\22000-20603.10.txt

Output Set: N:\CRF4\03172004\I208629G.raw

4 <110> APPLICANT: COUGHLIN, Shaun R.
 5 ISHIHARA, Hiroaki
 6 CONNOLLY, Andrew
 8 <120> TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR 3 AND USES
 9 THEREOF
 11 <130> FILE REFERENCE: 220002060310
 13 <140> CURRENT APPLICATION NUMBER: US 09/208,629G
 14 <141> CURRENT FILING DATE: 1998-12-08
 16 <150> PRIOR APPLICATION NUMBER: US 08/742,440
 17 <151> PRIOR FILING DATE: 1996-10-30
 19 <160> NUMBER OF SEQ ID NOS: 25
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1224
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Mus Musculus
 28 <400> SEQUENCE: 1
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 30 ttatcttggt tgcagctggg ctgctgtttc tgccagtcac tgtttgccaa agtggcataa 120
 31 atgtttcaga caactcagca aagccaacct taactattaa gagttttaat ggggggtcccc 180
 32 aaaatacctt tgaagaattc ccactttctg acatagaggg ctggacagga gccaccacaa 240
 33 ctataaaagc ggagtgtccc gaggacagta ttcaactct ccacgtgaat aatgctacca 300
 34 taggatacct gagaagttcc ttaagtaccc aagtgtacc tgccatctat atcctgctgt 360
 35 ttgtggttg tgtaccatcc aacatcgtga cctgtggaa actctcctta aggaccaa 420
 36 ccacagctct ggcatcttt cacaccaacc tggccatcgc agatctcctt ttctgtgtca 480
 37 cactgccatt taagatcgcc taccatctca atggcaacaa ctgggtattt ggcgaggtca 540
 38 tgtgccgat caccacggtc gttttctacg gcaacatgta ctgcgtatc ctgactctca 600
 39 cttgcatggg catcaaccgc tacctggcca cggctcacc ttccacatac cagaagctgc 660
 40 ccaaagcag cttctccttg ctcatgtgtg gcatagtgtg ggtcatggtt ttcttataca 720
 41 tgetgccctt tgtcatcctg aagcaggagt accacctcgt ccactcagag atcaccacct 780
 42 gccacgatgt cgtcgacgcg tgcgagtccc catcctcctt ccgattctac tacttcgtct 840
 43 ccttagcatt ctttgggttc ctcatcccgt ttgtgatcat catcttctgt tacacgactc 900
 44 tcatccacaa acttaaatca aaggatcgga tatggctggg ctacatcaag gccgtcctcc 960
 45 tcatccttgt gattttcaca atttgctttg cccccacaa catcactctc gtaatccacc 1020
 46 atgccaacta ctactaccac aataccgaca gcttgactt tatgtatctt attgctctgt 1080
 47 gcctggggag cctgaatagc tgccatagtc cattccttta ctttgtcatg tcgaaagttg 1140
 48 tagatcagct taatccttag tcggcaatgg caagaccact ttagagacca aggagagata 1200
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 51 <210> SEQ ID NO: 2
 52 <211> LENGTH: 1124
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Mus Musculus
 56 <220> FEATURE:

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57 <221> NAME/KEY: misc feature
 58 <222> LOCATION: (22) (27) 117, 118, 119, 120, 121, 122, 123, 350, 351, 442,
 59 443, 444, 595, 596, 597, 663, 785, 859, 860, 861, 862, 863,
 60 864

61 <223> OTHER INFORMATION: n = A, T, C, or G

63 <400> SEQUENCE: 2

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 65 caaccttaac tattaagagt ttttaatgggg gtccccaata tacctttgaa gaattcnnnn 120
 66 nnntacaact ctccatgtga ataatgctac catgggatac ctgagaagtt ccttaagtac 180
 67 caaagtgata cctgccatct acatcctggt gtttgtgatt ggtgtaccag cgaacatcgt 240
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 69 cctggccatc gcggatctcc tttctgtgt cagcgtgccg ttttaagatcn nccatccatc 360
 70 tcaatggcaa caactgggta tttggcgagg tcatgtgccg gatcaccacg gtcgttttct 420
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 74 caggagtacc acctcgtcca ctccgagatc accacctgcc acgatgtcgt cgacgcgtgc 660
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 77 gatcngatat ggtgtgggcta catcaaggcc gtcctctca tccttgtgaa tttcaccatc 840
 78 tgcttcccc ccaccaagnn nnnngatata tgggaagacg tacatgcttg gctgacttgt 900
 79 gcatggcacc atcagctcaa tttttaattt ttttaattta atttaattta attttatgtt 960
 80 tttgagacag agcctcactg tgtagtctg gctggcctgg ctggttctct atttagacca 1020
 81 ggtagcctt gaactcacag agatctgcct gcttctgcct cccaagtgt gggttcaacc 1080
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84 <210> SEQ ID NO: 3

85 <211> LENGTH: 369

86 <212> TYPE: PRT

87 <213> ORGANISM: Mus Musculus

89 <400> SEQUENCE: 3

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 92 Thr Val Cys Gln Ser Gly Ile Asn Val Ser Asp Asn Ser Ala Lys Pro
 93 20 25 30
 94 Thr Leu Thr Ile Lys Ser Phe Asn Gly Gly Pro Gln Asn Thr Phe Glu
 95 35 40 45
 96 Glu Phe Pro Leu Ser Asp Ile Glu Gly Trp Thr Gly Ala Thr Thr Thr
 97 50 55 60
 98 Ile Lys Ala Glu Cys Pro Glu Asp Ser Ile Ser Thr Leu His Val Asn
 99 65 70 75 80
 100 Asn Ala Thr Ile Gly Tyr Leu Arg Ser Ser Leu Ser Thr Gln Val Ile
 101 85 90 95
 102 Pro Ala Ile Tyr Ile Leu Leu Phe Val Val Gly Val Pro Ser Asn Ile
 103 100 105 110
 104 Val Thr Leu Trp Lys Leu Ser Leu Arg Thr Lys Ser Ile Ser Leu Val
 105 115 120 125
 106 Ile Phe His Thr Asn Leu Ala Ile Ala Asp Leu Leu Phe Cys Val Thr
 107 130 135 140
 108 Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe

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110 Gly Glu Val Met Cys Arg Ile Thr Thr Val Val Phe Tyr Gly Asn Met
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112 Tyr Cys Ala Ile Leu Ile Leu Thr Cys Met Gly Ile Asn Arg Tyr Leu
113          180          185          190
114 Ala Thr Ala His Pro Phe Thr Tyr Gln Lys Leu Pro Lys Arg Ser Phe
115          195          200          205
116 Ser Leu Leu Met Cys Gly Ile Val Trp Val Met Val Phe Leu Tyr Met
117          210          215          220
118 Leu Pro Phe Val Ile Leu Lys Gln Glu Tyr His Leu Val His Ser Glu
119 225          230          235          240
120 Ile Thr Thr Cys His Asp Val Val Asp Ala Cys Glu Ser Pro Ser Ser
121          245          250          255
122 Phe Arg Phe Tyr Tyr Phe Val Ser Leu Ala Phe Phe Gly Phe Leu Ile
123          260          265          270
124 Pro Phe Val Ile Ile Ile Phe Cys Tyr Thr Thr Leu Ile His Lys Leu
125          275          280          285
126 Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile Lys Ala Val Leu Leu
127          290          295          300
128 Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu
129 305          310          315          320
130 Val Ile His His Ala Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr
131          325          330          335
132 Phe Met Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu
133          340          345          350
134 Asp Pro Phe Leu Tyr Phe Val Met Ser Lys Val Val Asp Gln Leu Asn
135          355          360          365
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141 <211> LENGTH: 1224
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo Sapiens
145 <400> SEQUENCE: 4
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148 ggcattgaaa atgatacaaa caacttggca aagccaacct taccattaa gacctttcgt 180
149 ggagctcccc caaattcttt tgaagagttc cctttttctg ccttggagg ctggacagga 240
150 gccacgatta ctgtaaaaat taagtgcctt gaagaaagtg cttcacatct ccatgtgaaa 300
151 aatgctacca tgggttacct gaccagctcc ttaagtacta aactgatacc tgccatctac 360
152 ctccctggtg tttagattgg tgtcccgccc aatgctgtga cctgtggat gcttttcttc 420
153 aggaccagat ccattctgtac cactgtattc tacaccaacc tggccattgc agattttctt 480
154 ttttgtgtta cattgccctt taagatagct tatcatctca atgggaacaa ctgggtatgt 540
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156 ctgctccttg cctgcatcag catcaaccgc tacctggcca tegtccatcc ttccacctac 660
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158 ttcttatata tgctgccatt ttctactg aagcaggaat attatcttgt tcagccagac 780
159 atcaccacct gccatgatgt tcacaacact tgcgagtcct catctccctt ccaactctat 840
160 tacttcatct ccttggcatt ctttggattc ttaattccat ttgtgcttat catctactgc 900
161 tatgcagcca tcattccggac acttaatgca tacgatcata gatggttgtg gtatgttaag 960

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162 gcgagtctcc tcctccttgt gatttttacc atttgctttg ctccaagcaa tattattctt 1020
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164 atagctttgt gcctgggtag tcttaatagt tgcttagatc cattccttta ttttctcatg 1140
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169 <211> LENGTH: 1102
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo Sapiens
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176 ggagccacga ttactgtaa aattaagtgc cctgaagaaa gtgcttcaca tctccatgtg 180
177 aaaaatgcta ccatggggtg cctgaccagc tccttaagta ctaaactgat acctgccatc 240
178 tacctcctgg tgtttgtagt tgggtgtccg gccaatgctg tgacctgtg gatgctttt 300
179 ttcaggacca gatccatctg taccactgta ttctacacca acctggccat tgcagatttt 360
180 cttttttgtg ttacattgcc ctttaagata gcttatcatc tcaatgggaa caactgggta 420
181 tttggagagg tcctgtgccg ggcaccaca gtcattctt atggcaacat gtactgtctc 480
182 attctgtccc ttgcctgcat cagcatcaac cgctacctg ccactgtcca tctttcacc 540
183 taccggggcc tgcccaagca cacctatgcc ttggtaacat gtggactgg gtgggcaaca 600
184 gttttcttat atatgctgcc atttttcata ctgaagcagg aatattatct tgttcagcca 660
185 gacatcacca cctgccatga tgttcacaac acttgcgagt cctcatctcc cttccaactc 720
186 tattacttca tctccttggc attcttttga ttcttaatt catttgctg tatcatctac 780
187 tgctatgcag ccatcatccg gacacttaat gcatacgatc atagatgggt gtggtatggt 840
188 aaggcgagtc tcctcatcct tgtgatttt accatttgc ttgctccaag caatattatt 900
189 cttattattc accatgctaa ctactactac aacaacactg atggcttata ttttatatat 960
190 ctcatagctt tgtgcttgg tagtcttaat agttgcttag atccattcct ttattttctc 1020
191 atgtcaaaaa ccagaaatca ctccactgct taccttaca aatagtgaat tgatcttaga 1080
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195 <211> LENGTH: 374
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo Sapiens
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203 20 25 30
204 Pro Thr Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe
206 35 40 45
207 Glu Glu Phe Pro Phe Ser Ala Leu Glu Gly Trp Thr Gly Ala Thr Ile
208 50 55 60
209 Thr Val Lys Ile Lys Cys Pro Glu Glu Ser Ala Ser His Leu His Val
210 65 70 75 80
211 Lys Asn Ala Thr Met Gly Tyr Leu Thr Ser Ser Leu Ser Thr Lys Leu
212 85 90 95
213 Ile Pro Ala Ile Tyr Leu Leu Val Phe Val Val Gly Val Pro Ala Asn
214 100 105 110
215 Ala Val Thr Leu Trp Met Leu Phe Phe Arg Thr Arg Ser Ile Cys Thr

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216          115          120          125
217 Thr Val Phe Tyr Thr Asn Leu Ala Ile Ala Asp Phe Leu Phe Cys Val
218          130          135          140
219 Thr Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val
220 145          150          155          160
221 Phe Gly Glu Val Leu Cys Arg Ala Thr Thr Val Ile Phe Tyr Gly Asn
222          165          170          175
223 Met Tyr Cys Ser Ile Leu Leu Leu Ala Cys Ile Ser Ile Asn Arg Tyr
224          180          185          190
225 Leu Ala Ile Val His Pro Phe Thr Tyr Arg Gly Leu Pro Lys His Thr
226          195          200          205
227 Tyr Ala Leu Val Thr Cys Gly Leu Val Trp Ala Thr Val Phe Leu Tyr
228          210          215          220
229 Met Leu Pro Phe Phe Ile Leu Lys Gln Glu Tyr Tyr Leu Val Gln Pro
230 225          230          235          240
231 Asp Ile Thr Thr Cys His Asp Val His Asn Thr Cys Glu Ser Ser Ser
232          245          250          255
233 Pro Phe Gln Leu Tyr Tyr Phe Ile Ser Leu Ala Phe Phe Gly Phe Leu
234          260          265          270
235 Ile Pro Phe Val Leu Ile Ile Tyr Cys Tyr Ala Ala Ile Ile Arg Thr
236          275          280          285
237 Leu Asn Ala Tyr Asp His Arg Trp Leu Trp Tyr Val Lys Ala Ser Leu
238          290          295          300
239 Leu Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Ser Asn Ile Ile
240 305          310          315          320
241 Leu Ile Ile His His Ala Asn Tyr Tyr Tyr Asn Asn Thr Asp Gly Leu
242          325          330          335
243 Tyr Phe Ile Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys
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247 Thr Ala Tyr Leu Thr Lys
248          370
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252 <211> LENGTH: 425
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo Sapiens
256 <400> SEQUENCE: 7
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260          20          25          30
261 Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
262          35          40          45
263 Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
264          50          55          60
265 Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
266 65          70          75          80
267 Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 117,118,119,120,121,122,123,350,351,442,443,444,595,596,597
Seq#:2; N Pos. 663,785,859,860,861,862,863,864
Seq#:10; N Pos. 3,12,18,21,22,24,27
Seq#:11; N Pos. 6,9,12,15,21,24
Seq#:21; Xaa Pos. 1
Seq#:22; Xaa Pos. 1

VERIFICATION SUMMARY

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Input Set : A:\22000-20603.10.txt

Output Set: N:\CRF4\03172004\I208629G.raw

L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:60
M:341 Repeated in SeqNo=2
L:389 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:393 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:397 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:408 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:412 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:416 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:537 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:541 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:556 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:560 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0